What Is Claimed Is:

1. A compound composed of 11-24 amino acid residues comprising the amino acid sequence:

A_1-A_2-A_3-C_4-C_5-C_6-A_7-C_8-A_9-A_{10}-A_{11}-A_{12}-C_{13}-A_{14}-C_{15}-C_{16}-C_{17}-A_{18}

or a pharmaceutically acceptable salt or an N-terminal acylated or C-terminal amidated or esterified form thereof, said compound being either in a linear or in a disulfide-bridged form, wherein:

each of A_1-A_3 is independently present or not present, and if present each is independently a basic, hydrophobic, polar/large, or small amino acid;

each of C_4 and C_{17} is independently present or not present, and if present each is independently selected from the group consisting of cysteine, homocysteine, penicillamine, a basic amino acid, a hydrophobic amino acid, a polar/large amino acid and a small amino acid;

C_5 is selected from the group consisting of cysteine, homocysteine, penicillamine, a basic amino acid, a hydrophobic amino acid, a polar/large amino acid and a small amino acid;

each of C_6, C_8, C_{13} and C_{15} is independently selected from the group consisting of cysteine, homocysteine, penicillamine, a basic amino acid, a hydrophobic amino acid, a polar/large amino acid, a small amino acid and an acidic amino acid;

C_{16} is selected from the group consisting of cysteine, homocysteine, penicillamine, a hydrophobic amino acid or a small amino acid;

each of A_7 and A_{14} is independently a hydrophobic or a small amino acid;

A_9-A_{12} taken together are capable of effecting a β-turn when contained in the compound and at least one of A_9-A_{12} is a basic amino acid;

A_{18} is present or not present, and if present, is a basic, hydrophobic, polar/large, or small amino acid;

at least about 15% to about 50% of the amino acid residues composing said compound are basic amino acids; and

said compound has a net positive charge of at least +1 at physiological pH;

with the provisos that: (i) when one of C_4, C_5 or C_6 is cysteine, homocysteine or penicillamine, the other two are other than cysteine, homocysteine and penicillamine;

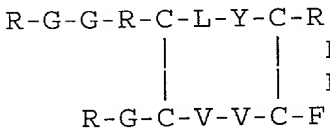
(ii) when one of C_{15}, C_{16} or C_{17} is cysteine, homocysteine or penicillamine, the other two are other than cysteine, homocysteine and penicillamine;

and (iii) at least one of C_4, C_5, C_{16} or C_{17} is cysteine, homocysteine or penicillamine.

2. The compound of claim 1 which comprises two disulfide bridges.

3. The compound of Claim 2, wherein one of said disulfide bridges links C_5-C_{16} and the other links C_8-C_{13}.

4. The compound of Claim 3 which is selected from the group consisting of: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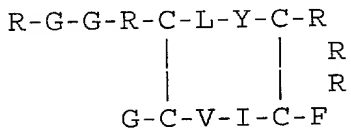
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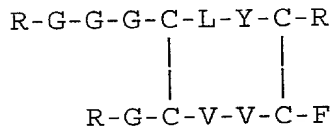
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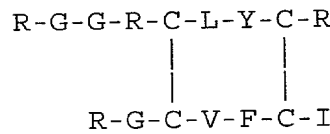
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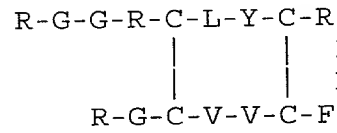
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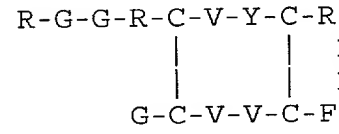
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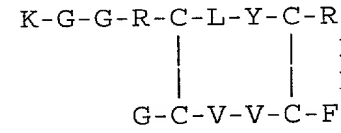
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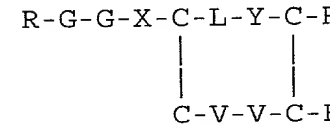
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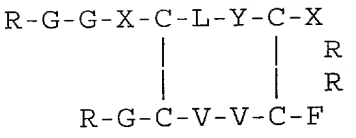

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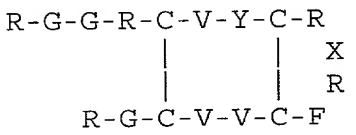

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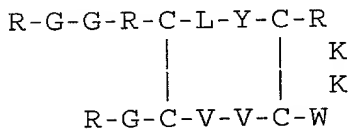

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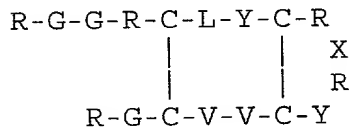

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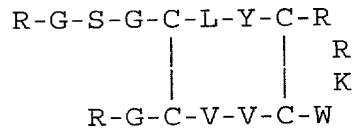

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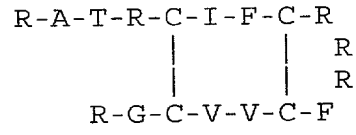

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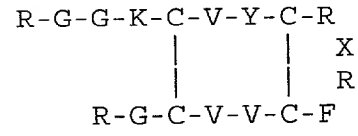

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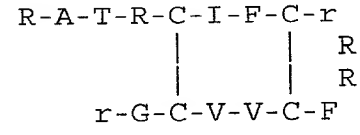

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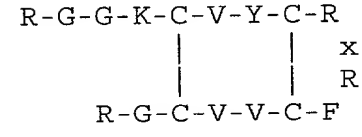

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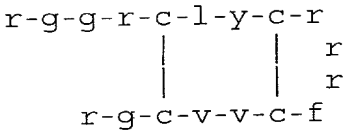

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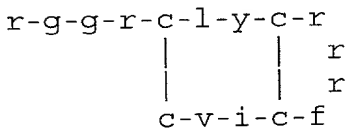

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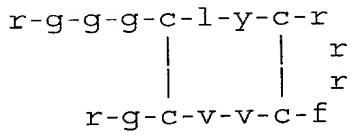

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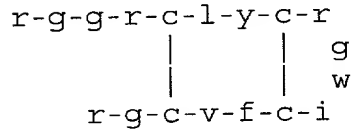


(SEQ ID NO:124);

and the C-terminal amidated forms thereof, wherein X is Har, x is D-Har, lower case letters represent D-amino acids and lines between C or c residues represent disulfide linkages.

5. The compound of Claim 2, wherein one of said disulfide bridges links C_5-C_8 and the other links C_{13}-C_{16}.

6. The compound of Claim 5 which is selected from the group consisting of:

(SEQ ID NO:125);

(SEQ ID NO:126);


RGGGCLYCRRRFCVVCGR (SEQ ID NO:127);


RGGRCLYCRGWICFVCGR (SEQ ID NO:128);


RGGRCLYCRPRFCVVCGR (SEQ ID NO:129);


RGGRCVYCRRRFCVVCG (SEQ ID NO:130);


KGGRCLYCRRRFCVVCG (SEQ ID NO:131);


RGGXCLYCRRRFCVVC (SEQ ID NO:132);


RGGXCLYCXRRFCVVCGR (SEQ ID NO:133);


RGGRCVYCRXRFCVVCGR (SEQ ID NO:134);


RGGRCLYCRKKWCVVCGR (SEQ ID NO:135);


RGGRCLYCRXRYCVVCGR (SEQ ID NO:136);


RGSGCLYCRRKWCVVCGR (SEQ ID NO:137);

RATRCIFCRRRFCVVCGR (SEQ ID NO:138);

RGGKCVYCRXRFCVVCGR (SEQ ID NO:139);

RATRCIFCrRRFCVVCGr (SEQ ID NO:140);

RGGKCVYCRxRFCVVCGR (SEQ ID NO:141);

rggrclycrrrfcvvcgr (SEQ ID NO:142);

rggrclycrrrfcivcg (SEQ ID NO:143);

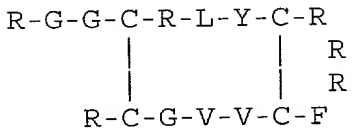
rgggclycrrrfcvvcgr (SEQ ID NO:144);

RGGRCLYCRGWICFVCGR (SEQ ID NO:145);

and the C-terminal amidated forms thereof, wherein X is Har, x is D-Har, lower case letters represent D-amino acids and lines between C and c residues represent disulfide linkages.

7. The compound of Claim 2, wherein one of said disulfide bridges links C_4-C_{17} and the other links C_8-C_{13}.

8. The compound of Claim 7 which is selected from the group consisting of: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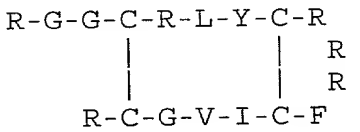
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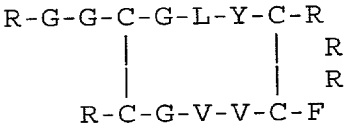
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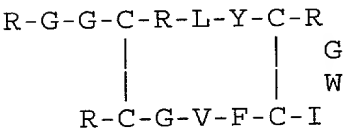
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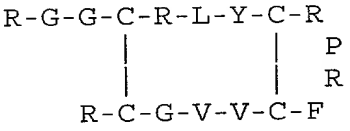
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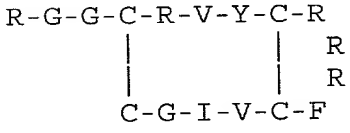
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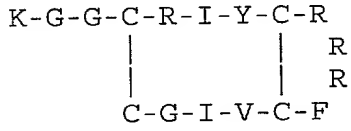
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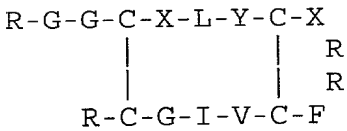
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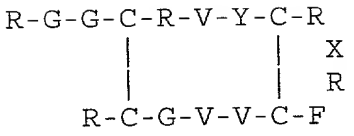
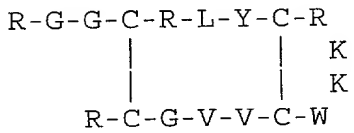


(SEQ ID NO:149);



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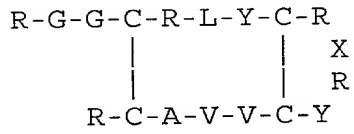

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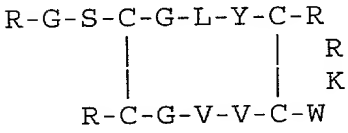

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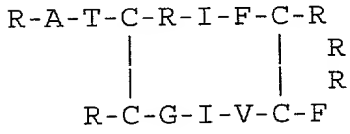

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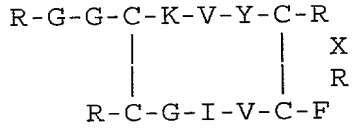

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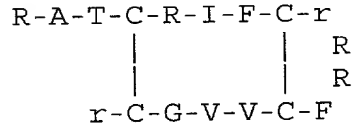

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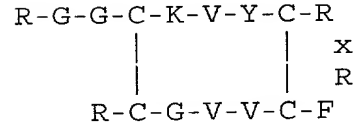

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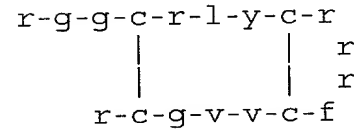

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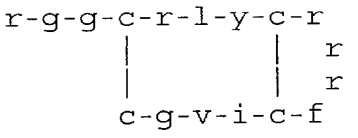

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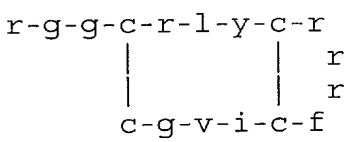

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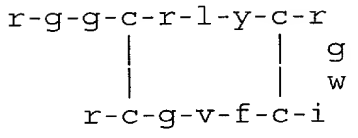

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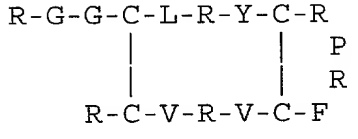

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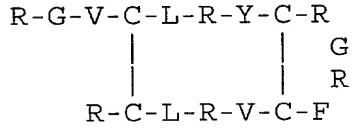

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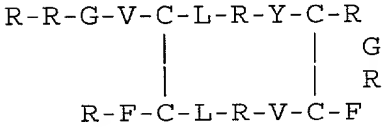

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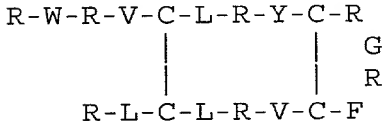

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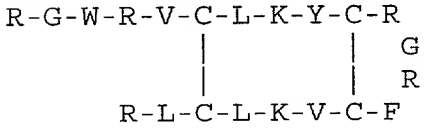

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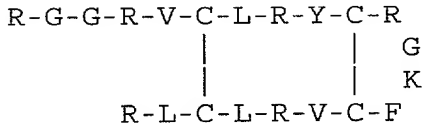

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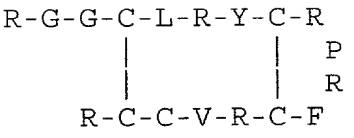
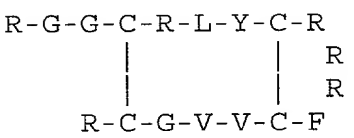
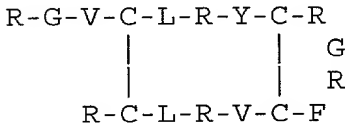


(SEQ ID NO:167);



(SEQ ID NO:168);



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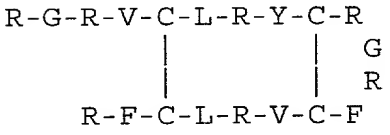
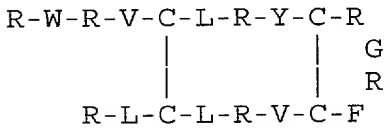
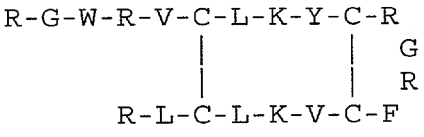


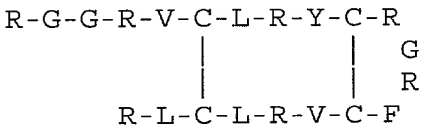
(SEQ ID NO:170);



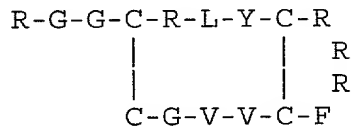
(SEQ ID NO:171);



(SEQ ID NO:172);



(SEQ ID NO:173);



(SEQ ID NO:174)

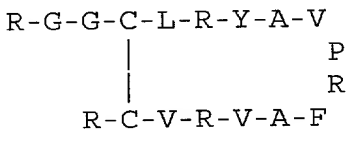
and the C-terminal amidated forms thereof, wherein X is Har, x is D-Har, lower case letters represent D-amino acids

and lines between C or c residues represent disulfide linkages.

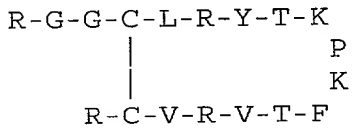
9. The compound of Claim 1 which comprises one disulfide bridge.

10. The compound of Claim 9 in which said disulfide bridge links C_4-C_{17}.

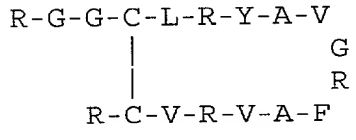
11. The compound of Claim 10 which is selected from the group consisting of:



(SEQ ID NO:175);



(SEQ ID NO:176);



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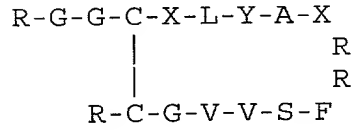
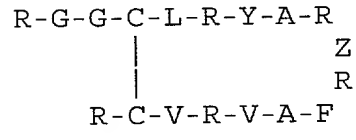
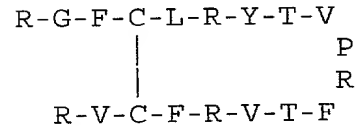


(SEQ ID NO:178);



(SEQ ID NO:179);



(SEQ ID NO:180);

```
R-G-F-C-L-R-Y-K-V
      |           G
      |           R
  R-V-C-F-R-V-K-F
```
(SEQ ID NO:181);

```
R-G-F-C-L-R-Y-Z-V
      |           G
      |           R
  R-V-C-F-R-V-Z-F
```
(SEQ ID NO:182);

```
R-G-G-C-L-R-Y-A-R
      |           Z
      |           R
    R-C-V-R-V-A-F
```
(SEQ ID NO:183);

```
R-G-G-C-L-R-Y-A-V
      |           G
      |           R
    R-C-V-R-V-A-F
```
(SEQ ID NO:184);

and the C-terminal amidated forms thereof, wherein X is Har, Z is MeGly and lines between C residues represent disulfide linkages.

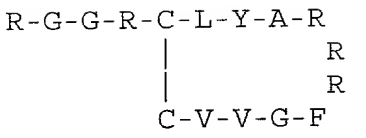
12. The compound of Claim 9 in which said disulfide bridge links C_5-C_{16}.

13. The compound of Claim 12 which is selected from the group consisting of:

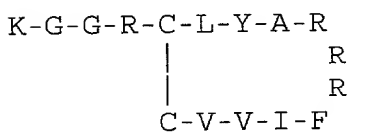
```
R-G-G-R-C-L-Y-A-R
      |           R
      |           R
    R-G-C-V-V-A-F
```
(SEQ ID NO:185);

```
R-G-G-R-C-L-Y-A-R
      |           R
      |           R
      C-V-I-S-F
```
(SEQ ID NO:186);

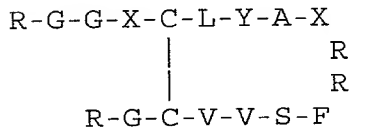
```
R-G-G-G-C-L-Y-S-R
      |           R
      |           R
    R-G-C-V-V-A-F
```
(SEQ ID NO:187);



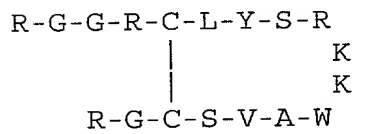
(SEQ ID NO:188);



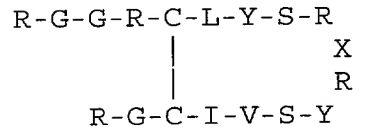
(SEQ ID NO:189);



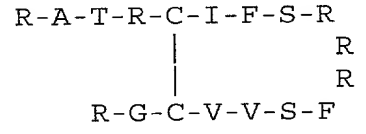
(SEQ ID NO:190);



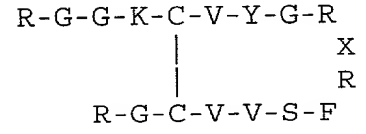
(SEQ ID NO:191);



(SEQ ID NO:192);



(SEQ ID NO:193);



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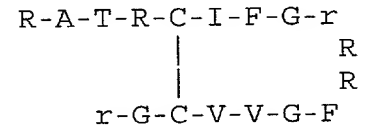

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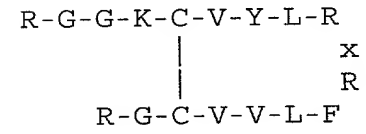
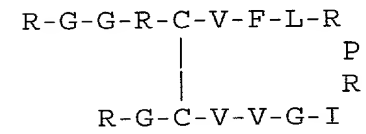


(SEQ ID NO:196);



(SEQ ID NO:197);

and the C-terminal amidated forms thereof, wherein X is Har, x is D-Har, lower case letters represent D-amino acids and lines between C residues represent disulfide linkages.

14. The compound of Claim 9 in which the disulfide bridge links C_8 and C_{13}.

15. The compound of Claim 1 which is in the linear form.

16. The compound of Claim 1 in which at least one of A_1, A_2 or A_3 is not present.

17. The compound Claim 1 in which A_1, A_2 and A_3 are not present.

18. The compound of Claim 1 in which at least one of A_1, A_2 or A_3 is a hydrophobic amino acid.

19. The compound of Claim 1 in which each of C_5 and C_{16} is independently selected from the group consisting of cysteine, homocysteine, penicillamine, I, V, L, NLe, W, Y, F, A, S, G and T.

20. The compound of Claim 1 in which each of C_4 and C_{17} is independently selected from the group consisting of cysteine, homocysteine, penicillamine, I, V, L, NLe, W, Y, F, A, S, G and T.

21. The compound of Claim 1 in which each of A_7 and A_{14} is independently selected from the group consisting of I, V, L, NLe, W, Y, F, A, S, G and T.

22. The compound of Claim 1 in which one of A_9 or A_{12} is R, K, Har, Orn or H and the other is I, V, L, NLe, W, Y, F, A, S, G or T.

23. The compound of Claim 1 in which all amino acids are in the D-configuration.

24. The compound of Claim 1 in which A_7 and A_{14} are each independently a hydrophobic amino acid.

25. The compound of Claim 1 in which A_9 or A_{12} is a hydrophobic amino acid or a small amino acid.

26. The compound of Claim 1 in which A_{10} and A_{11} are each independently selected from the group consisting of proline, a basic amino acid, a hydrophobic amino acid and a small amino acid.

27. The compound of Claim 1 in which each of C_8 and C_{13} is independently cysteine, homocysteine or penicillamine.

28. The compound of Claim 1 in which A_9-A_{10}-A_{11}-A_{12} is selected from the group consisting of: R-R-R-F, R-G-W-I, R-P-R-F, X-R-R-F, R-X-RF, R-K-K-W, R-X-R-Y, R-R-K-W, r-R-R-F, R-x-R-F, R-G-R-F, C-R-G-R, Y-C-G-R, V-P-R-F, K-P-K-F,

V-G-R-F, R-P-R-I and R-Z-R-F, where X is Har, x is D-Har, Z is MeGly and r is D-Arg.

29. The compound of Claim 1 which is in the linear or disulfide-bridged form and which is selected from the group consisting of:

RGGRCLYCRRRFCVVCGR (SEQ ID NO:11);
RGGCRLYCRRRFCVVGCR (SEQ ID NO:12);
RGGRCLYCRRRFCIVCG (SEQ ID NO:13);
RGGCRLYCRRRFCIVGC (SEQ ID NO:14);
RGGGCLYCRRRFCVVCGR (SEQ ID NO:15);
RGGCGLYCRRRFCVVGCR (SEQ ID NO:16);
RGGRCLYCRGWICFVCGR (SEQ ID NO:17);
RGGCRLYCRGWICFVGCR (SEQ ID NO:18);
RGGRCLYCRPRFCVVCGR (SEQ ID NO:19);
RGGCRLYCRPRFCVVGCR (SEQ ID NO:20);
RGGRCVYCRRRFCVVCG (SEQ ID NO:21);
RGGCRVYCRRRFCVIGC (SEQ ID NO:22);
KGGRCLYCRRRFCVVCG (SEQ ID NO:23);
KGGCRIYCRRRFCVIGC (SEQ ID NO:24);
RGGXCLYCRRRFCVVC (SEQ ID NO:25);
RGGCXLYCRRRFCVIC (SEQ ID NO:26);
RGGXCLYCXRRFCVVCGR (SEQ ID NO:27);
RGGCXLYCXRRFCVIGCR (SEQ ID NO:28);
RGGRCVYCRXRFCVVCGR (SEQ ID NO:29);
RGGCRVYCRXRFCVVGCR (SEQ ID NO:30);
RGGRCLYCRKKWCVVCGR (SEQ ID NO:31);
RGGCRLYCRKKWCVVGCR (SEQ ID NO:32);
RGGRCLYCRXRYCVVCGR (SEQ ID NO:33);
RGGCRLYCRXRYCVVACR (SEQ ID NO:34);

RGSGCLYCRRKWCVVCGR (SEQ ID NO:35);

RGSCGLYCRRKWCVVGCR (SEQ ID NO:36);

RATRCIFCRRRFCVVCGR (SEQ ID NO:37);

RATCRIFCRRRFCVIGCR (SEQ ID NO:38);

RGGKCVYCRXRFCVVCGR (SEQ ID NO:39);

RGGCKVYCRXRFCVIGCR (SEQ ID NO:40);

RATRCIFCrRRFCVVCGr (SEQ ID NO:41);

RATCRIFCrRRFCVVGCr (SEQ ID NO:42);

RGGKCVYCRxRFCVVCGR (SEQ ID NO:43);

RGGCKVYCRxRFCVVGCR (SEQ ID NO:44);

rggrclycrrrfcvvcgr (SEQ ID NO:45);

rggcrlycrrrfcvvgcr (SEQ ID NO:46);

rggrclycrrrfcivcg (SEQ ID NO:47);

rggcrlycrrrfcivgc (SEQ ID NO:48);

rgggclycrrrfcvvcgr (SEQ ID NO:49);

rggcglycrrrfcvvgcr (SEQ ID NO:50);

rggrclycrgwicfvcgr (SEQ ID NO:51);

rggcrlycrgwicfvgcr (SEQ ID NO:52);

RGGCLRYCRPRFCVRVCR (SEQ ID NO:53);

RGGCRLYCRRRFCVVGCR (SEQ ID NO:54);

RGVCLRYCRGRFCVRLCR (SEQ ID NO:55);

RGRVCLRYCRGRFCVRLCFR (SEQ ID NO:56);

RWRVCLRYCRGRFCVRLCLR (SEQ ID NO:57);

RGWRVCLKYCRGRFCVKLCLR (SEQ ID NO:58);

RGGRVCLRYCRGKFCVRLCLR (SEQ ID NO:59);

RGGRCLYARRRFAVVCGR (SEQ ID NO:60);

RGGRCLYARRRFSIVC (SEQ ID NO:61);

RGGGCLYSRRRFAVVCGR (SEQ ID NO:62);

RGGRCLYARRRFGVVC (SEQ ID NO:63);

KGGRCLYVRRRFIVVC (SEQ ID NO:64);

RGGXCLYARRRFVGCV (SEQ ID NO:65);

RGGXCLYAXRRFSVVCR (SEQ ID NO:66);

RGGCXLYAXRRFSVVGCR (SEQ ID NO:67);

RGGRCVYVRXRFLVCVGR (SEQ ID NO:68);

RGGRCLYSRKKWAVSCGR (SEQ ID NO:69);

RGGRCLYSRXRYSVICGR (SEQ ID NO:70);

RGSGCIYCRRKWGVVGCR (SEQ ID NO:71);

RATRCIFSRRRFSVVCGR (SEQ ID NO:72);

RGGKCVYGRXRFSVVCGR (SEQ ID NO:73);

RATRCIFGrRRFGVVCGr (SEQ ID NO:74);

RGGKCVYLRxRFLVVCGR (SEQ ID NO:75);

RGGRCVFLRPRIGVVCGR (SEQ ID NO:76);

RGGCLRYAVPRFAVRVCR (SEQ ID NO:77);

RGGCLRYTKPKFTVRVCR (SEQ ID NO:78);

RGGCLRYAVGRFAVRVCR (SEQ ID NO:79);

RGGCLRYARZRFAVRVCR (SEQ ID NO:80);

RGFCLRYTVPRFTVRFCVR (SEQ ID NO:81);

RGFCLRYKVGRFKVRFCVR (SEQ ID NO:82);

RGFCLRYZVGRFZVRFCVR (SEQ ID NO:83);

RGGCLRYARZRFAVRVCR (SEQ ID NO:84);

RGGCLRYAVGRFAVRVCR (SEQ ID NO:85);

RGGRCLYCRRRFCVVGCR (SEQ ID NO:86);

RGGCRLYCRRRFCVVCGR (SEQ ID NO:87);

RGGRCLYCRRRFCVCVGR (SEQ ID NO:88);

RGGCRLYCRRRFCVCVGR (SEQ ID NO:89);

RGGRLCYCRRRFCVVCGR (SEQ ID NO:90);

RGGRLCYCRRRFCVVGCR (SEQ ID NO:91);

RGGCRLYCRRRFCVVGC (SEQ ID NO:92);

RGGRCLYCRRRFCVVGC (SEQ ID NO:93);

RGGCRLYCRRRFCVVCG (SEQ ID NO:94);

RGGRCLYCRRRFCVCVG (SEQ ID NO:95);

RGGCRLYCRRRFCVCVG (SEQ ID NO:96);

RGGRLCYCRRRFCVVCG (SEQ ID NO:97);

RGGRLCYCRRRFCVVGC (SEQ ID NO:98);

RGGGCLYCRRRFCVVGCR (SEQ ID NO:99);

RGGGCLYCRRRFCVCVGR (SEQ ID NO:100);

RGGCGLYCRRRFCVCVGR (SEQ ID NO:101);

RGGGLCYCRRRFCVVCGR (SEQ ID NO:102);

RGGGLCYCRRRFCVVGCR (SEQ ID NO:103);

and the C-terminal amidated and N-terminal acylated forms thereof, wherein X is Har, x is D-Har, Z is MeGly and lower case letters represent D-amino acids.

30. A pharmaceutical composition comprising a compound according to Claim 1 and a pharmaceutically acceptable excipient.

31. A method of inhibiting the growth of a microbe or the replication of a virus which comprises the step of contacting said virus or said microbe with an amount of a compound according to Claim 1 effective to inhibit said growth or said replication.

32. The method of Claim 31 in which the microbe is a bacteria.

33. The method of Claim 32 in which the bacteria is selected from the group consisting of E. coli, L. monocytogenes, B. subtilis, S. typhimurium, S. aureus and P. aeruginosa.

34. The method of Claim 31 in which the microbe or virus is a sexually-transmitted microbe or virus.

35. The method of Claim 34 in which the sexually-transmitted microbe or virus is selected from the group consisting of HIV-1, C. trachomatis, T. pallidum, N. gonorrhoeae, T. vaginalis, HSV-1, HSV-2, H. ducreyi and human papilloma virus.

36. The method of Claim 31 in which the microbe or virus is HIV.

37. The method of Claim 31 in which the microbe or virus is methicillin-resistant S. aureus (MRSA) or vancomycin-resistant E. faecalis (VREF).

38. A method to inactivate the endotoxin of gram-negative bacteria, which method comprises contacting said endotoxin with an amount of a compound according to Claim 1 effective to inactivate said endotoxin.

39. A method to treat or prevent a microbial or viral infection in a subject, which method comprises administering to a subject in need of such treatment an amount of a compound according to Claim 1 effective to ameliorate said infection in the subject.

40. The method of Claim 39 in which the infection is a bacterial infection.

41. The method of Claim 40 in which the bacteria is selected from the group consisting of E. Coli, L. monocytogenes, B. subtilis, S. typhimurium, S. aureus and P. aeruginosa.

42. The method of Claim 39 in which the infection is caused by a sexually-transmitted pathogen.

43. The method of Claim 42 in which the sexually-transmitted pathogen is selected from the group consisting of HIV-1, C. trachomatis, T. pallidum, N. gonorrhoeae, T. vaginalis, HSV-1, HSV-2, H. ducreyi and human papilloma virus.

44. The method of Claim 39 in which the infection is an HIV infection.

45. The method of Claim 39 in which the infection is a methicillin-resistant S. aureus (MRSA) or vancomycin-resistant E. faecalis (VREF) infection.

46. The method of Claim 39 in which the compound is administered topically.

47. The method of Claim 39 in which the compound is administered prophylactically.